



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

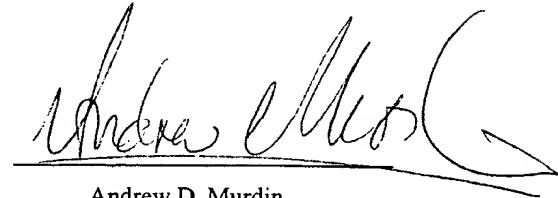
Applicant : Andrew D. MURDIN, et al.
Appln. No. : 09/662,812
Filed: September 15, 2000
Title : Chlamydia Antigens and Corresponding DNA Fragments
And Uscs Thrcrof
Grp./A.U. : 1645
Examiner : Virginia A Portner
Docket No. : 77813-27

DECLARATION PURSUANT TO 37 CFR § 1.132

I, ANDREW D. MURDIN, hereby declare that:

1. I am a co-inventor of the subject matter described and claimed in the above-identified application, and I am therefore familiar with and understand its content.
2. Example 3 at pages 50-51 of the specification describes the immunization of mice against *Chlamydia pneumoniae* infection with a plasmid containing the coding sequence of *C. pneumoniae* protein pCAmgp002 (i.e. SEQ ID NO: 2), as well as the same plasmid vector containing a non related control sequence pCABk917.
3. Open reading frame pCABk917 is a hypothetical outer membrane protein that is not related to open reading frame pCAmgp002. Attached hereto as Appendix 1 are the results of a comparison between the protein sequences of pCAmgp002 and pCABk917. Not only are the proteins of different lengths (568 amino acids vs 344 amino acids) but they also have very little homology to each other as seen in Appendix I..
4. Importantly, the data presented in Appendix 1 hereto demonstrate that open reading frames pCAmgp002 and pCABk917 are in fact very different proteins and would not be expected to show the same protective ability in the mouse model described in Example 3.
5. I hereby declare that all statements made herein of my knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false

statements and the like are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of this application or any patent issuing thereon.



Andrew D. Murdin

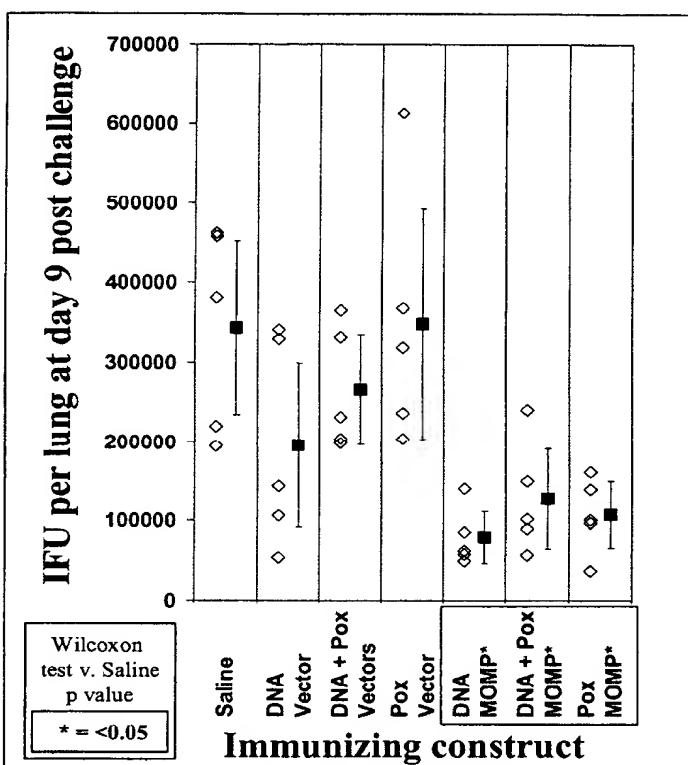
3rd Sept 2003

Date

Appendix I

BEST AVAILABLE COPY

Figure 1.



BEST AVAIL ALIGN

Appendix I

BESTFIT of: cabk917.pep check: 8099 from: 1 to: 344
to: mop002.pep check: 3837 from: 1 to: 568

Symbol comparison table: blosum62.cmp CompCheck: 1102
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad.
Sci. USA 89: 10915-10919.

Gap Weight: 8 Average Match: 2.778
Length Weight: 2 Average Mismatch: -2.248
Quality: 36 Length: 61
Ratio: 0.667 Gaps: 2
Percent Similarity: 42.593 Percent Identity: 27.778

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

cabk917.pep x mop002.pep August 28, 2003 14:23 ..

126 CVFATIALQETSPAAIPLLIAFTARVGGLK...QYYRLP....LNAYRD 168
418 CIVYKLLASQKTQLATTIAISFLSHTSHQEALDLLFQAAKLPGEPIIRAYAD 467
169 FTSNPLNAESE 179
468 LAIYNLTKDPE 478